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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=10; day=29; hr=14; min=2; sec=36; ms=339;]

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Reviewer Comments:

<210> 3

<211> 6

<212> PRT

<213> artificial

<220>

<223> distinctive fragment

<400> 3

Ile Ala Arg Ile Ile Gly

1 5

The above <223> response is an insufficient explanation for "Artificial Sequence": please give more information regarding the source of the "distinctive fragment." Same type of insufficient explanations in Sequences 4-11.

Application No: 10578493

Version No: 3.0

Input Set:

Output Set:

Started: 2008-09-29 16:55:12.825

Finished: 2008-09-29 16:55:14.100

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 275 ms

Total Warnings: 32

Total Errors: 0

No. of SeqIDs Defined: 36

Actual SeqID Count: 36

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Input Set:

Output Set:

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Actual SeqID Count: 36

Error code

Error Description

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SEQUENCE LISTING

<110> Desire, Laurent

<120> BACE455, AN ALTERNATIVE SPLICE VARIANT OF THE HUMAN
BETA-SECRETASE

<130> 67987.000002

<140> 10578493

<141> 2006-05-05

<150> PCT/IB2004/003897

<151> 2004-11-05

<150> 60/517,401

<151> 2003-11-03

<160> 36

<170> PatentIn version 3.5

<210> 1

<211> 1368

<212> DNA

<213> Homo sapiens

<400> 1

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 <213> Homo sapiens

<400> 2

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Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr	Asp
	35						40					45			

Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val
	50					55					60				

Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr
65					70					75				80	

Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser
				85					90					95	

Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr
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Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val
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Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile	145	150	155	160
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Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Ile	Ile	Gly	180	185	190	
Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	195	200	205	
Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	210	215	220	
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Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	275	280	285	
Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	290	295	300	
Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	305	310	315	320
Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	325	330	335	
Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	340	345	350	

Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
355 360 365

Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala
370 375 380

Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn
385 390 395 400

Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met
405 410 415

Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys
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Asp Asp Ile Ser Leu Leu Lys
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<210> 3

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<213> artificial

<220>

<223> distinctive fragment

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<210> 4

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20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Cys Ala Gly Phe Pro Leu Asn Gln

210	215	220
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Asp His Ser Leu Tyr Thr	Gly Ser Leu Trp Tyr Thr	Pro Ile Arg Arg
245	250	255
Glu Trp Tyr Tyr Glu Val Ile Ile	Val Arg Val Glu Ile	Asn Gly Gln
260	265	270
Asp Leu Lys Met Asp Cys Lys Glu Tyr	Asn Tyr Asp Lys Ser Ile Val	
275	280	285
Asp Ser Gly Thr Thr Asn Leu Arg Leu	Pro Lys Lys Val Phe Glu Ala	
290	295	300
Ala Val Lys Ser Ile Lys Ala Ala Ser Ser	Thr Glu Lys Phe Pro Asp	
305	310	315 320
Gly Phe Trp Leu Gly Glu Gln Leu Val	Cys Trp Gln Ala Gly Thr Thr	
325	330	335
Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu	Met Gly Glu Val	
340	345	350
Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro	Gln Gln Tyr Leu Arg	
355	360	365
Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp	Cys Tyr Lys Phe Ala	
370	375	380
Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val	Ile Met Glu	
385	390	395 400
Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg	Ile Gly Phe Ala	
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Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr	Ala Ala Val Glu	
420	425	430
Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr	Asn Ile Pro	
435	440	445

Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
450 455 460

Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
465 470 475 480

Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp
485 490 495

Ile Ser Leu Leu Lys
500